



sequence listing US 10507446.txt  
SEQUENCE LISTING

GOTO, Hidetsugu  
NAKANO, Shigeru

<120> GENE PARTICIPATING IN ACETIC ACID TOLERANCE, ACETIC ACID BACTERIA  
BRED USING THE GENE, AND PROCESS FOR PRODUCING VINEGAR WITH THE  
USE OF THE ACETIC ACID BACTERIA

<130> 4439-4024

<140> US/10/507,446

<141> 2004-09-13

<150> PCT/JP03/02946

<151> 2003-03-12

<160> 10

<170> PatentIn version 3.2..

<210> 1

<211> 2016

<212> DNA

<213> Gluconacetobacter entanii

<400> 1

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gatatccgca ccattgatga tctggctgcc tgtatcgtct ctctcaagca ggcattcctga	180
tacaccatgt cgattttctc gaaatatgaa ggccttgctg cgccttgctc ggccggtaacg	240
gccgatggtg ggcgcaaccc gttcaacgct gtgatcgaag agccatttct ctccacggctc	300
gggctgatcg aagggcgca gacgcttctg ttcggcacca acaactatct tgggctgagc	360
cagtccccgg ccgcatcga agcggcggtg gaagccgcca gggcttatgg tgcgggcacg	420
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gccagcatct atgatggcag ccgccttggc catgcgcagg tcatccgctt ccgtcacaac	660
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gccgtcaagc gggaaaccgg tgcatggctg ctggcggtg aagcacattc cgttggtgta	840
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gccgggctgg acctgatccg gctgtgttcg cgtccgtaca tggtcaccgc atccctgccg	1020
ccggaagtca tcgccgcgac catggccgcg ctgactgaac tggaaaaccg gccggaactg	1080

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cgcggtgcggt tgatggacaa tgcacgcagg cttcatgacg ggctgcaggc ggccggcctg 1140  
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 ccaccgcgcg gataatgcag gccaggatgg catcggccgc gtccggttcc ctgaccata 1920  
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<210> 2  
 <211> 400  
 <212> PRT  
 <213> Gluconacetobacter entanii

<400> 2

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Val Thr Ala Asp Gly Gly Arg Asn Pro Phe Asn Val Val Ile Glu Lys  
 20 25 30

Pro Ile Ser Ser Thr Val Gly Leu Ile Glu Gly Arg Glu Thr Leu Leu  
 35 40 45

Phe Gly Thr Asn Asn Tyr Leu Gly Leu Ser Gln Ser Pro Ala Ala Ile  
 50 55 60

Glu Ala Ala Val Glu Ala Ala Arg Ala Tyr Gly Val Gly Thr Thr Gly  
 65 70 75 80

Ser Arg Ile Ala Asn Gly Thr Gln Gly Leu His Arg Gln Leu Glu Glu  
 85 90 95

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Arg Leu Cys Thr Phe Phe Arg Arg Arg His Cys Met Val Phe Ser Thr  
100 105 110

Gly Tyr Gln Ala Asn Leu Gly Thr Ile Ser Ala Leu Ala Gly Lys Asp  
115 120 125

Asp Tyr Leu Leu Leu Asp Ala Asp Ser His Ala Ser Ile Tyr Asp Gly  
130 135 140

Ser Arg Leu Gly His Ala Gln Val Ile Arg Phe Arg His Asn Asp Ala  
145 150 155 160

Asp Asp Leu His Lys Arg Leu Arg Arg Leu Asp Gly Thr Pro Gly Ala  
165 170 175

Lys Leu Val Val Val Glu Gly Ile Tyr Ser Met Met Gly Asp Val Val  
180 185 190

Pro Met Ala Glu Phe Ala Ala Val Lys Arg Glu Thr Gly Ala Trp Leu  
195 200 205

Leu Ala Asp Glu Ala His Ser Val Gly Val Met Gly Glu His Gly Arg  
210 215 220

Gly Val Ala Glu Ser Asp Gly Val Glu Asp Asp Val Asp Phe Val Val  
225 230 235 240

Gly Thr Phe Ser Lys Ser Leu Gly Thr Val Gly Gly Tyr Cys Val Ser  
245 250 255

Asn His Ala Gly Leu Asp Leu Ile Arg Leu Cys Ser Arg Pro Tyr Met  
260 265 270

Phe Thr Ala Ser Leu Pro Pro Glu Val Ile Ala Ala Thr Met Ala Ala  
275 280 285

Leu Thr Glu Leu Glu Asn Arg Pro Glu Leu Arg Val Arg Leu Met Asp  
290 295 300

Asn Ala Arg Arg Leu His Asp Gly Leu Gln Ala Ala Gly Leu Arg Thr  
305 310 315 320

Gly Pro Gln Ala Ser Pro Val Val Ser Val Ile Leu Asp Asp Val Ala  
325 330 335

Val Ala Val Ala Phe Trp Asn Arg Leu Leu Asp Leu Gly Val Tyr Val  
340 345 350

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Asn Leu Ser Leu Pro Pro Ala Thr Pro Asp Gln His Pro Leu Leu Arg  
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Thr Ser Val Met Ala Thr His Thr Pro Glu Gln Ile Asp Arg Ala Val  
370 375 380

Glu Ile Phe Ala Val Val Ala Gly Glu Met Gly Ile Asn Arg Ala Ala  
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<211> 1360  
<212> DNA  
<213> Acetobacter aceti

<400> 3  
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atattccaaa tttgaaggta cggcaggcgc gctgggttcc gttgtggccg taggcggtcg 180  
caaccctttt gctgttggtta ttgaaaaacc tgtctcttca actggttgaa ttattgaagg 240  
tcgggaaacg cttctttttg gcaccaataa ctatttgggg cttagtcaat ccaaaaatgc 300  
cattcaagca gcccagcagg ctgccgcggc atgtggcgta ggcacaacgg gctcacgcat 360  
tgcaaatggc acacaatccc tgcaccgaca gcttgaaaaa gatattgccg cgtttttttg 420  
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gctggcaggt aaggatgacc acctgtttct ggatgctgat agccacgcca gtatctatga 540  
tggcagccgc ctgagtgcag cagaagttat tcgcttccgc cataatgatc cagacaacct 600  
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gcggccggtg ctccgttggt ccgtaatggc caccatacgc cccgaacaaa ttgcgcaggc 1260  
tattgccata ttcaggcagg ctgcggcaga agtaggcgta accatcacac cctccgctgc 1320

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1360

<210> 4  
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<212> PRT  
<213> Acetobacter aceti  
<400> 4

Met Thr Ser Leu Phe Ser Lys Phe Glu Gly Thr Ala Gly Ala Leu Gly  
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20 25 30

Lys Pro Val Ser Ser Thr Val Gly Ile Ile Glu Gly Arg Glu Thr Leu  
35 40 45

Leu Phe Gly Thr Asn Asn Tyr Leu Gly Leu Ser Gln Ser Lys Asn Ala  
50 55 60

Ile Gln Ala Ala Gln Gln Ala Ala Ala Ala Cys Gly Val Gly Thr Thr  
65 70 75 80

Gly Ser Arg Ile Ala Asn Gly Thr Gln Ser Leu His Arg Gln Leu Glu  
85 90 95

Lys Asp Ile Ala Ala Phe Phe Gly Arg Arg Asp Ala Met Val Phe Ser  
100 105 110

Thr Gly Tyr Gln Ala Asn Leu Gly Ile Ile Ser Thr Leu Ala Gly Lys  
115 120 125

Asp Asp His Leu Phe Leu Asp Ala Asp Ser His Ala Ser Ile Tyr Asp  
130 135 140

Gly Ser Arg Leu Ser Ala Ala Glu Val Ile Arg Phe Arg His Asn Asp  
145 150 155 160

Pro Asp Asn Leu Tyr Lys Arg Leu Lys Arg Met Asp Gly Thr Pro Gly  
165 170 175

Ala Lys Leu Ile Val Val Glu Gly Ile Tyr Ser Met Thr Gly Asn Val  
180 185 190

Ala Pro Ile Ala Glu Phe Val Ala Val Lys Lys Glu Thr Gly Ala Tyr  
195 200 205

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Leu Leu Val Asp Glu Ala His Ser Phe Gly Val Leu Gly Gln Asn Gly  
210 215 220

Arg Gly Ala Ala Glu Ala Asp Gly Val Glu Ala Asp Val Asp Phe Val  
225 230 235 240

Val Gly Thr Phe Ser Lys Ser Leu Gly Thr Val Gly Gly Tyr Cys Val  
245 250 255

Ser Asp His Pro Glu Leu Glu Phe Val Arg Leu Asn Cys Arg Pro Tyr  
260 265 270

Met Phe Thr Ala Ser Leu Pro Pro Glu Val Ile Ala Ala Thr Thr Ala  
275 280 285

Ala Leu Lys Asp Met Gln Ala His Pro Glu Leu Arg Lys Gln Leu Met  
290 295 300

Ala Asn Ala Gln Gln Leu His Ala Gly Phe Val Asp Ile Gly Leu Asn  
305 310 315 320

Ala Ser Lys His Ala Thr Pro Val Ile Ala Val Thr Leu Glu Thr Ala  
325 330 335

Glu Glu Ala Ile Pro Met Trp Asn Arg Leu Leu Glu Leu Gly Val Tyr  
340 345 350

Val Asn Leu Ser Leu Pro Pro Ala Thr Pro Asp Ser Arg Pro Leu Leu  
355 360 365

Arg Cys Ser Val Met Ala Thr His Thr Pro Glu Gln Ile Ala Gln Ala  
370 375 380

Ile Ala Ile Phe Arg Gln Ala Ala Ala Glu Val Gly Val Thr Ile Thr  
385 390 395 400

Pro Ser Ala Ala

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<220>  
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<223> synthetic primer

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acggctgcag ctggtctgcc tgccgtatct 30

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sequence listing US 10507446.txt

<210> 10  
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cagccttcct ccggctacac cagattcgc

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